



#10

SEQUENCE LISTING

<110> Messier, Walter

Sikela, James M

<120> Methods to Identify Polynucleotide and Polypeptide
Sequences Which May Be Associated with Physiological
and Medical Conditions

<130> GENO2002CIP2

<140>

<141>

<150> 09/591,435

<151> 2000-06-09

<150> 09/240,915

<151> 1999-01-29

<150> 60/073,263

<151> 1998-01-30

<150> 60/098,987

<151> 1998-09-02

<150> 09/942,252

<151> 2001-08-28

<170> PatentIn Ver. 2.0

<210> 1

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 1

cagacatctg tgtccccctc aaaagtcac cgtccccggg gaggtccgt gctggtgaca 60
tgcagcacct cctgtgacca gcccaagttg ttgggcatag agaccccggt gcctaaaaag 120
gagttgctcc tgctgggaa caaccggaag gtgtatgaac tgagcaatgt gcaagaagat 180
agccaaccaa tgtgtatttc aaactgcctt gatgggcagt caacagctaa aaccttcctc 240
accgtgtact ggactccaga acgggtggaa ctggcacccc tccctctttg gcagccagtg 300
ggcaagaacc ttaccctacg ctgccaggtg gaggtgggg caccocgggc caacctcacc 360
gtggtgctgc tccgtgggga gaaggagctg aaacgggagc cagctgtggg ggagcccgt 420
gaggtcacga ccacggtgct ggtgaggaga gatcaccatg gagccaattt ctggtgccgc 480
actgaactgg acctgcggcc ccaagggtg gagctgtttg agaacacctc ggccccctac 540
cagctccaga cctttgtcct gccagcgact cccccacaac ttgtcagccc ccgggtccta 600
gaggtggaca cgcaggggac cgtggtctgt tccctggacg ggtgttccc agtctcggag 660

gcccaggtcc acctggcact gggggaccag aggttgaacc ccacagtcac ctatggcaac 720

gactccttct cggccaaggc ctcagtcagt gtgaccgcag aggacgaggg caccagcg 780

ctgacgtgtg cagtaatact ggggaaccag agccaggaga cactgcagac agtgaccatc 840

tacagctttc cggcgcccaa cgtgattctg acgaagccag aggtctcaga agggaccgag 900

gtgacagtga agtgtgaggc ccaccctaga gccaaggtga cgctgaatgg ggttccagcc 960

cagccactgg gcccgagggc ccagctcctg ctgaaggcca cccagagga caacgggagc 1020

agcttctcct gctctgcaac cctggaggtg gccggccagc ttatacaca gaaccagacc 1080

cgggagcttc gtgtcctgta tggccccga ctggacgaga gggattgtcc gggaaactgg 1140

acgtggccag aaaattcca gcagactcca atgtgccagg cttgggggaa cccattgccc 1200

gagctcaagt gtctaaagga tggcactttc ccactgccca tcggggaatc agtgactgtc 1260

actcgagatc ttgagggcac ctacctctgt cgggccagga gcactcaagg ggaggtcacc 1320

cgcgaggtga ccgtgaatgt gctctcccc cggtatgaga ttgtcatcat cactgtggta 1380

gcagccgcag tcataatggg cactgcaggc ctcagcacgt acctctataa ccgccagcg 1440

aagatcaaga aatacagact acaacaggcc caaaaaggga ccccatgaa accgaacaca 1500

caagccacgc ctccctga 1518

<210> 2

<211> 1518

<212> DNA

<213> Pan troglodytes

<220>

<221> CDS

<222> (1)..(1518)

<400> 2

cag aca tct gtg tcc ccc cca aaa gtc atc ctg ccc cgg gga ggc tcc 48

Gln Thr Ser Val Ser Pro Pro Lys Val Ile Leu Pro Arg Gly Gly Ser .

1 5 10 15

gtg cag gtg aca tgc agc acc tcc tgt gac cag ccc gac ttg ttg ggc 96

Val Gln Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Asp Leu Leu Gly

20 25 30

ata gag acc ccg ttg cct aaa aag gag ttg ctt ctg ggt ggg aac aac 144

Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Gly Gly Asn Asn

35 40 45

tgg aag gtg tat gaa ctg agc aat gtg caa gaa gat agc caa cca atg 192

Trp Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met

50 55 60

tgc tat tca aac tgc cct gat ggg cag tca aca gct aaa acc ttc ctc 240

Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu

65 70 75 80

acc gtg tac tgg act cca gaa cgg gtg gaa ctg gca ccc ctc ccc tct	288
Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser	
85 90 95	
tgg cag cca gtg ggc aag gac ctt acc cta cgc tgc cag gtg gag ggt	336
Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly	
100 105 110	
ggg gca ccc cgg gcc aac ctc acc gtg gtg ctg ctc cgt ggg gag aag	384
Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys	
115 120 125	
gag ctg aaa cgg gag cca gct gtg ggg gag ccc gct gag gtc acg acc	432
Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr	
130 135 140	
acg gtg ctg gtg gag aga gat cac cat gga gcc aat ttc tcg tgc cgc	480
Thr Val Leu Val Glu Arg Asp His His Gly Ala Asn Phe Ser Cys Arg	
145 150 155 160	
act gaa ctg gac ctg cgg ccc caa ggg ctg cag ctg ttt gag aac acc	528
Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Gln Leu Phe Glu Asn Thr	
165 170 175	
tcg gcc ccc cac cag ctc caa acc ttt gtc ctg cca gcg act ccc cca	576
Ser Ala Pro His Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro	
180 185 190	
caa ctt gtc agc ccc cgg gtc cta gag gtg gac acg cag ggg acc gtg	624
Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val	
195 200 205	

gtc tgt tcc ctg gac ggg ctg ttc cca gtc tcg gag gcc cag gtc cac	672
Val Cys Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His	
210 215 220	
ctg gca ctg ggg gac cag agg ttg aac ccc aca gtc acc tat ggc aat	720
Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn	
225 230 235 240	
gac tcc ttc tcg gcc aag gcc tca gtc agt gtg acc gca gag gac gag	768
Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu	
245 250 255	
ggc acc cag cgg ctg acg tgt gca gta ata ctg ggg aac cag agc cgg	816
Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Arg	
260 265 270	
gag aca ctg cag aca gtg acc atc tac agc ttt ccg gcg ccc aac gtg	864
Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val	
275 280 285	
att ctg acg aag cca gag gtc tca gaa ggg acc gag gtg aca gtg aag	912
Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys	
290 295 300	
tgt gag gcc cac cct aga gcc aag gtg acg ctg aat ggg gtt cca gcc	960
Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala	
305 310 315 320	
cag cca gtg ggc ccg agg gtc cag ctc ctg ctg aag gcc acc cca gag	1008

Gln Pro Val Gly Pro Arg Val Gln Leu Leu Leu Lys Ala Thr Pro Glu	
325	330 335
gac aac ggg cgc agc ttc tcc tgc tct gca acc ctg gag gtg gcc ggc	1056
Asp Asn Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly	
340	345 350
cag ctt ata cac aag aac cag acc cgg gag ctt cgt gtc ctg tat ggc	1104
Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly	
355	360 365
ccc cga ctg gac gag agg gat tgt ccg gga aac tgg acg tgg cca gaa	1152
Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu	
370	375 380
aat tcc cag cag act cca atg tgc cag gct tcg ggg aac cca ttg ccc	1200
Asn Ser Gln Gln Thr Pro Met Cys Gln Ala Ser Gly Asn Pro Leu Pro	
385	390 395 400
gag ctc aag tgt cta aag gat ggc act ttc cca ctg ccc gtc ggg gaa	1248
Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Val Gly Glu	
405	410 415
tca gtg act gtc act cga gat ctt gag ggc acc tac ctc tgt cgg gcc	1296
Ser Val Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala	
420	425 430
agg agc act caa ggg gag gtc acc cgc aag gtg acc gtg aat gtg ctc	1344
Arg Ser Thr Gln Gly Glu Val Thr Arg Lys Val Thr Val Asn Val Leu	
435	440 445

tcc ccc cgg tat gag att gtc atc atc act gtg gta gca gcc gca gtc 1392
 Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val
 450 455 460

ata atg ggc act gca ggc ctc agc acg tac ctc tat aac cgc cag cgg 1440
 Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg
 465 470 475 480

aag atc agg aaa tac aga cta caa cag gct caa aaa ggg acc ccc atg 1488
 Lys Ile Arg Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met
 485 490 495

aaa ccg aac aca caa gcc acg cct ccc tga 1518
 Lys Pro Asn Thr Gln Ala Thr Pro Pro
 500 505

<210> 3

<211> 505

<212> PRT

'<213> Pan troglodytes

<400> 3

Gln Thr Ser Val Ser Pro Pro Lys Val Ile Leu Pro Arg Gly Gly Ser
 1 5 10 15

Val Gln Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Asp Leu Leu Gly
 20 25 30

Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Gly Gly Asn Asn

35

40

45

Trp Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met
50 55 60

Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu
65 70 75 80

Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser
85 90 95

Trp Gln Pro Val Gly Lys Asp Leu Thr Leu Arg Cys Gln Val Glu Gly
100 105 110

Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys
115 120 125

Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr
130 135 140

Thr Val Leu Val Glu Arg Asp His His Gly Ala Asn Phe Ser Cys Arg
145 150 155 160

Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Gln Leu Phe Glu Asn Thr
165 170 175

Ser Ala Pro His Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro
180 185 190

Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val
195 200 205

Val Cys Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His
210 215 220

Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn
225 230 235 240

Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu
245 250 255

Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Arg
260 265 270

Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val
275 280 285

Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys
290 295 300

Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala
305 310 315 320

Gln Pro Val Gly Pro Arg Val Gln Leu Leu Leu Lys Ala Thr Pro Glu
325 330 335

Asp Asn Gly Arg Ser Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly
340 345 350

Gln Leu Ile His Lys Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly
355 360 365

Pro Arg Leu Asp Glu Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu
370 375 380

Asn Ser Gln Gln Thr Pro Met Cys Gln Ala Ser Gly Asn Pro Leu Pro
385 390 395 400

Glu Leu Lys Cys Leu Lys Asp Gly Thr Phe Pro Leu Pro Val Gly Glu
405 410 415

Ser Val Thr Val Thr Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala
420 425 430

Arg Ser Thr Gln Gly Glu Val Thr Arg Lys Val Thr Val Asn Val Leu
435 440 445

Ser Pro Arg Tyr Glu Ile Val Ile Ile Thr Val Val Ala Ala Ala Val
450 455 460

Ile Met Gly Thr Ala Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg
465 470 475 480

Lys Ile Arg Lys Tyr Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met
485 490 495

Lys Pro Asn Thr Gln Ala Thr Pro Pro
500 505

<210> 4

<211> 1515

<212> DNA

<213> Gorilla gorilla

<400> 4

cagacatctg tgtcccccc aaaagtcac ctgccccggg gaggtccgt gctggtgaca 60

tgcagcacct cctgtgacca gccaccttg ttgggcatag agaccccggt gcctaaaaag 120

gagttgctcc tgcttgggaa caaccagaag gtgtatgaac tgagcaatgt gcaagaagat 180

agccaaccaa tgtgttattc aaactgccct gatgggcagt caacagctaa aaccttcctc 240

accgtgtact ggactccaga acgggtggaa ctggcacccc tcccctcttg gcagccagtg 300

ggcaaggacc ttaccctacg ctgccagggt gaggggtggg caccgcgggc caacatcatc 360

gtggtgctgc tccgtgggga ggaggagctg aaacgggagc cagctgtggg ggagcccgcc 420

gaggtcacga ccacggtgcc ggtggagaaa gatcaccatg gagccaattt cttgtgccgc 480

actgaactgg acctgcggcc ccaagggtg aagctgtttg agaacacctc ggccccctac 540

cagctccaaa ctttgcct gccagcgact ccccaaac ttgtcagccc tcgggtccta 600

gaggtggaca cgcaggggac tgtggtctgt tccctggacg ggctgttccc agtctcgag 660

gccaggtcc acctggcact gggggaccag aggttgaacc ccacagtcac ctatggcaac 720

gactccttct cagccaaggc ctcatcagt gtgaccgcag aggacgagg caccagtggt 780

ctgacgtgtg cagtaatact ggggacccag agccaggaga cactgcagac agtgaccatc 840
 tacagctttc cggcacccaa cgtgattctg acgaagccag aggtctcaga agggaccgag 900
 gtgacagtga agtgtgaggc ccaccctaga gccaaaggta cactgaatgg ggttccagcc 960
 cagccaccgg gcccgaggac ccagttcctg ctgaaggcca cccagagga caacgggcgc 1020
 agcttctcct gctctgcaac cctggagggtg gccggccagc ttatacaca gaaccagacc 1080
 cgggagcttc gtgtcctgta tggccccga ctggatgaga gggattgtcc gggaaactgg 1140
 acgtggccag aaaattccca gcagactcca atgtgccagg cttgggggaa ccattgccc 1200
 gagctcaagt gtctaaagga tggcactttc ccactgcccg tcggggaatc agtgactgtc 1260
 actcgagatc ttgagggcac ctacctctgt cgggccagga gcactcaagg ggaggtcacc 1320
 cgcgagggtga ccgtgaatgt gctctcccc cggtatgagt ttgtcatcat cgctgtgta 1380
 gcagccgcag tcataatggg cactgcaggc ctcagcacgt acctctataa ccgccagcgg 1440
 aagatcagga aatacagact acaacaggct caaaaaggga ccccatgaa accgaacaca 1500
 caagccacgc ctccc 1515

<210> 5

<211> 1515

<212> DNA

<213> Pongo pygmaeus

<400> 5

cacacatctg tgtcctccgc caacgtcttc ctgccccggg gaggctccgt gctagtgaat 60

tgcagcacct cctgtgacca gccaccttg ttgggcatag agaccccggt gcctaaaaag 120

gagttgctcc cgggtgggaa caactggaag atgtatgaac tgagcaatgt gcaagaagat 180

agccaaccaa tgtgctattc aaactgccct gatgggcagt cagcagctaa aaccttcctc 240

accgtgtact ggactccaga acgggtggaa ctggcacccc tcccctcttg gcagccagtg 300

ggcaagaacc ttaccctacg ctgccaggtg gaggggtggg caccctgggc caacctcacc 360

gtggtattgc tccgtgggga ggaggagctg agccggcagc cagcgggtggg ggagcccgcc 420

gaggtcacgg ccacggtgct ggcgaggaaa gatgaccacg gagccaattt ctcgtgccgc 480

actgaactgg acctgcggcc ccaagggctg gagctgtttg agaacacctc ggccccccac 540

cagctccaaa cctttgtcct gccagcgact cccccacaac ttgtcagccc ccgggtccta 600

gaggtggaca cgcaggggac cgtggtctgt tccctggacg ggctgttccc agtctcggag 660

gccaggtcc acttggcact gggggaccag aggttgaacc ccacagtcac ctatggcgtc 720

gactccctct cggccaaggc ctcagtcagt gtgaccgcag aggaggaggg caccagtggt 780

ctgtggtgtg cagtgatact gaggaaccag agccaggaga cacggcagac agtgaccatc 840

tacagctttc ctgcacccaa cgtgactctg atgaagccag aggtctcaga agggaccgag 900
 gtgatagtga agtgtgaggg ccaccctgca gccaacgtga cgctgaatgg ggttccagcc 960
 cagccgcccgg gcccgagggc ccagttcctg ctgaaggcca cccagagga caacgggccc 1020
 agcttctcct gctctgcaac cctggaggtg gccggccagc ttatacaca gaaccagacc 1080
 cgggagcttc gagtctgtga tggccccga ctggacgaga gggattgtcc gggaaactgg 1140
 acgtggccag aaaactccca gcagactcca atgtgccagg cttgggggaa ccccttgccc 1200
 gagctcaagt gtctaaagga tggcactttc ccactgccca tcggggaatc agtgactgtc 1260
 actcgagatc ttgagggcac ctacctctgt cgggccagga gcactcaagg ggaggtcacc 1320
 cgcgaggtga ccgtgaatgt gctctcccc cggtatgaga ttgtcatcat cactgtggta 1380
 gcagccgcag ccatactggg cactgcaggg ctcagcacgt acctctataa ccgccagcgg 1440
 aagatcagga tatacagact acaacaggct caaaaaggga ccccatgaa accaaacaca 1500
 caaaccacgc ctccc 1515

<210> 6

<211> 505

<212> PRT

<213> Homo sapiens

<400> 6

Gln	Thr	Ser	Val	Ser	Pro	Ser	Lys	Val	Ile	Leu	Pro	Arg	Gly	Gly	Ser
1				5					10					15	
Val	Leu	Val	Thr	Cys	Ser	Thr	Ser	Cys	Asp	Gln	Pro	Lys	Leu	Leu	Gly
			20					25				30			
Ile	Glu	Thr	Pro	Leu	Pro	Lys	Lys	Glu	Leu	Leu	Leu	Pro	Gly	Asn	Asn
			35				40					45			
Arg	Lys	Val	Tyr	Glu	Leu	Ser	Asn	Val	Gln	Glu	Asp	Ser	Gln	Pro	Met
	50						55					60			
Cys	Tyr	Ser	Asn	Cys	Pro	Asp	Gly	Gln	Ser	Thr	Ala	Lys	Thr	Phe	Leu
65					70					75					80
Thr	Val	Tyr	Trp	Thr	Pro	Glu	Arg	Val	Glu	Leu	Ala	Pro	Leu	Pro	Ser
				85					90					95	
Trp	Gln	Pro	Val	Gly	Lys	Asn	Leu	Thr	Leu	Arg	Cys	Gln	Val	Glu	Gly
			100					105					110		
Gly	Ala	Pro	Arg	Ala	Asn	Leu	Thr	Val	Val	Leu	Leu	Arg	Gly	Glu	Lys
		115					120					125			
Glu	Leu	Lys	Arg	Glu	Pro	Ala	Val	Gly	Glu	Pro	Ala	Glu	Val	Thr	Thr
	130					135					140				
Thr	Val	Leu	Val	Arg	Arg	Asp	His	His	Gly	Ala	Asn	Phe	Ser	Cys	Arg
145					150					155					160

Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr
165 170 175

Ser Ala Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro
180 185 190

Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val
195 200 205

Val Cys Ser Leu Asp Gly Leu Phe Pro Val Ser Glu Ala Gln Val His
210 215 220

Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn
225 230 235 240

Asp Ser Phe Ser Ala Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu
245 250 255

Gly Thr Gln Arg Leu Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln
260 265 270

Glu Thr Leu Gln Thr Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val
275 280 285

Ile Leu Thr Lys Pro Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys
290 295 300

Cys Glu Ala His Pro Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala
305 310 315 320

Gln Pro Leu Gly Pro Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu

	325		330		335										
Asp	Asn	Gly	Arg	Ser	Phe	Ser	Cys	Ser	Ala	Thr	Leu	Glu	Val	Ala	Gly
	340		345		350										
Gln	Leu	Ile	His	Lys	Asn	Gln	Thr	Arg	Glu	Leu	Arg	Val	Leu	Tyr	Gly
	355		360		365										
Pro	Arg	Leu	Asp	Glu	Arg	Asp	Cys	Pro	Gly	Asn	Trp	Thr	Trp	Pro	Glu
	370		375		380										
Asn	Ser	Gln	Gln	Thr	Pro	Met	Cys	Gln	Ala	Trp	Gly	Asn	Pro	Leu	Pro
385			390		395									400	
Glu	Leu	Lys	Cys	Leu	Lys	Asp	Gly	Thr	Phe	Pro	Leu	Pro	Ile	Gly	Glu
	405		410		415										
Ser	Val	Thr	Val	Thr	Arg	Asp	Leu	Glu	Gly	Thr	Tyr	Leu	Cys	Arg	Ala
	420		425		430										
Arg	Ser	Thr	Gln	Gly	Glu	Val	Thr	Arg	Glu	Val	Thr	Val	Asn	Val	Leu
	435		440		445										
Ser	Pro	Arg	Tyr	Glu	Ile	Val	Ile	Ile	Thr	Val	Val	Ala	Ala	Ala	Val
	450		455		460										
Ile	Met	Gly	Thr	Ala	Gly	Leu	Ser	Thr	Tyr	Leu	Tyr	Asn	Arg	Gln	Arg
465			470		475									480	
Lys	Ile	Lys	Lys	Tyr	Arg	Leu	Gln	Gln	Ala	Gln	Lys	Gly	Thr	Pro	Met

485

490

495

Lys Pro Asn Thr Gln Ala Thr Pro Pro

500

505

<210> 7

<211> 254

<212> PRT

<213> Homo sapiens

<400> 7

Ser Asp Glu Lys Val Phe Glu Val His Val Arg Pro Lys Lys Leu Ala

1

5

10

15

Val Glu Pro Lys Gly Ser Leu Glu Val Asn Cys Ser Thr Thr Cys Asn

20

25

30

Gln Pro Glu Val Gly Gly Leu Glu Thr Ser Leu Asp Lys Ile Leu Leu

35

40

45

Asp Glu Gln Ala Gln Trp Lys His Tyr Leu Val Ser Asn Ile Ser His

50

55

60

Asp Thr Val Leu Gln Cys His Phe Thr Cys Ser Gly Lys Gln Glu Ser

65

70

75

80

Met Asn Ser Asn Val Ser Val Tyr Gln Pro Pro Arg Gln Val Ile Leu

85

90

95

Thr Leu Gln Pro Thr Leu Val Ala Val Gly Lys Ser Phe Thr Ile Glu

	100		105		110
Cys Arg Val Pro Thr Val Glu Pro Leu Asp Ser Leu Thr Leu Phe Leu					
	115		120		125
Phe Arg Gly Asn Glu Thr Leu His Tyr Glu Thr Phe Gly Lys Ala Ala					
	130		135		140
Pro Ala Pro Gln Glu Ala Thr Ala Thr Phe Asn Ser Thr Ala Asp Arg					
145		150		155	160
Glu Asp Gly His Arg Asn Phe Ser Cys Leu Ala Val Leu Asp Leu Met					
	165		170		175
Ser Arg Gly Gly Asn Ile Phe His Lys His Ser Ala Pro Lys Met Leu					
	180		185		190
Glu Ile Tyr Glu Pro Val Ser Asp Ser Gln Met Val Ile Ile Val Thr					
	195		200		205
Val Val Ser Val Leu Leu Ser Leu Phe Val Thr Ser Val Leu Leu Cys					
	210		215		220
Phe Ile Phe Gly Gln His Leu Arg Gln Gln Arg Met Gly Thr Tyr Gly					
225		230		235	240
Val Arg Ala Ala Trp Arg Arg Leu Pro Gln Ala Phe Arg Pro					
	245		250		

<210> 8

<211> 518

<212> PRT

<213> Homo sapiens

<400> 8

Gln Glu Phe Leu Leu Arg Val Glu Pro Gln Asn Pro Val Leu Ser Ala

1 5 10 15

Gly Gly Ser Leu Phe Val Asn Cys Ser Thr Asp Cys Pro Ser Ser Glu

20 25 30

Lys Ile Ala Leu Glu Thr Ser Leu Ser Lys Glu Leu Val Ala Ser Gly

35 40 45

Met Gly Trp Ala Ala Phe Asn Leu Ser Asn Val Thr Gly Asn Ser Arg

50 55 60

Ile Leu Cys Ser Val Tyr Cys Asn Gly Ser Gln Ile Thr Gly Ser Ser

65 70 75 80

Asn Ile Thr Val Tyr Gly Leu Pro Glu Arg Val Glu Leu Ala Pro Leu

85 90 95

Pro Pro Trp Gln Pro Val Gly Gln Asn Phe Thr Leu Arg Cys Gln Val

100 105 110

Glu Gly Gly Ser Pro Arg Thr Ser Leu Thr Val Val Leu Leu Arg Trp

115 120 125

Glu Glu Glu Leu Ser Arg Gln Pro Ala Val Glu Glu Pro Ala Glu Val

130	135	140	
Thr Ala Thr Val Leu Ala Ser Arg Asp Asp His Gly Ala Pro Phe Ser			
145	150	155	160
Cys Arg Thr Glu Leu Asp Met Gln Pro Gln Gly Leu Gly Leu Phe Val			
	165	170	175
Asn Thr Ser Ala Pro Arg Gln Leu Arg Thr Phe Val Leu Pro Val Thr			
	180	185	190
Pro Pro Arg Leu Val Ala Pro Arg Phe Leu Glu Val Glu Thr Ser Trp			
	195	200	205
Pro Val Asp Cys Thr Leu Asp Gly Leu Phe Pro Ala Ser Glu Ala Gln			
	210	215	220
Val Tyr Leu Ala Leu Gly Asp Gln Met Leu Asn Ala Thr Val Met Asn			
225	230	235	240
His Gly Asp Thr Leu Thr Ala Thr Ala Thr Ala Thr Ala Arg Ala Asp			
	245	250	255
Gln Glu Gly Ala Arg Glu Ile Val Cys Asn Val Thr Leu Gly Gly Glu			
	260	265	270
Arg Arg Glu Ala Arg Glu Asn Leu Thr Val Phe Ser Phe Leu Gly Pro			
	275	280	285
Ile Val Asn Leu Ser Glu Pro Thr Ala His Glu Gly Ser Thr Val Thr			

290	295	300	
Val Ser Cys Met Ala Gly Ala Arg Val Gln Val Thr Leu Asp Gly Val			
305	310	315	320
Pro Ala Ala Ala Pro Gly Gln Pro Ala Gln Leu Gln Leu Asn Ala Thr			
	325	330	335
Glu Ser Asp Asp Gly Arg Ser Phe Phe Cys Ser Ala Thr Leu Glu Val			
	340	345	350
Asp Gly Glu Phe Leu His Arg Asn Ser Ser Val Gln Leu Arg Val Leu			
	355	360	365
Tyr Gly Pro Lys Ile Asp Arg Ala Thr Cys Pro Gln His Leu Lys Trp			
	370	375	380
Lys Asp Lys Thr Arg His Val Leu Gln Cys Gln Ala Arg Gly Asn Pro			
385	390	395	400
Tyr Pro Glu Leu Arg Cys Leu Lys Glu Gly Ser Ser Arg Glu Val Pro			
	405	410	415
Val Gly Ile Pro Phe Phe Val Asn Val Thr His Asn Gly Thr Tyr Gln			
	420	425	430
Cys Gln Ala Ser Ser Ser Arg Gly Lys Tyr Thr Leu Val Val Val Met			
	435	440	445
Asp Ile Glu Ala Gly Ser Ser His Phe Val Pro Val Phe Val Ala Val			
	450	455	460

Leu Leu Thr Leu Gly Val Val Thr Ile Val Leu Ala Leu Met Tyr Val
465 470 475 480

Phe Arg Glu His Gln Arg Ser Gly Ser Tyr His Val Arg Glu Glu Ser
485 490 495

Thr Tyr Leu Pro Leu Thr Ser Met Gln Pro Thr Glu Ala Met Gly Glu
500 505 510

Glu Pro Ser Arg Ala Glu
515

<210> 9

<211> 1212

<212> DNA

<213> Homo sapiens

<400> 9

atgagtgact ccaaggaacc aagactgcag cagctgggcc tcctggagga ggaacagctg 60

agaggccttg gattccgaca gactcgagga tacaagagct tagcaggggtg tcttggccat 120

ggccccctgg tgctgcaact cctctccttc acgctcttgg ctgggctcct tgtccaagtg 180

tccaaggtec ccagctccat aagtcaggaa caatccaggc aagacgcgat ctaccagaac 240

ctgacccagc ttaaagctgc agtgggtgag ctctcagaga aatccaagct gcaggagatc 300

taccaggagc tgaccagct gaaggctgca gtgggtgagc ttccagagaa atctaagctg 360

caggagatct accaggagct gaccggctg aaggctgcag tgggtgagct tccagagaaa 420

tctaagctgc aggagatcta ccaggagctg acctggctga aggctgcagt gggtagctt 480

ccagagaaat ctaagatgca ggagatctac caggagctga ctcggtgaa ggctgcagtg 540

ggtagcttc cagagaaatc taagcagcag gagatctacc aggagctgac ccggctgaag 600

gctgcagtgg gtgagcttcc agagaaatct aagcagcagg agatctacca ggagctgacc 660

cggtgaagg ctgcagtggg tgagcttcca gagaaatcta agcagcagga gatctaccag 720

gagctgaccc agctgaaggc tgcagtggaa cgctgtgcc acccctgtcc ctgggaatgg 780

acattcttcc aaggaaactg ttacttcatg tctaactccc agcggaactg gcacgactcc 840

atcaccgcct gcaaagaagt gggggcccag ctctcgttaa taaaagtgc tgaggagcag 900

aacttcctac agctgcagtc ttccagaagt aaccgcttca cctggatggg actttcagat 960

ctaaatcagg aaggcacgtg gcaatgggtg gacggctcac ctctgttgcc cagcttcaag 1020

cagtattgga acagaggaga gcccaacaac gttggggagg aagactgcgc ggaatttagt 1080

ggcaatggct ggaacgacga caaatgtaat cttgccaaat tctggatctg caaaaagtcc 1140

gcagcctcct gctccaggga tgaagaacag tttctttctc cagccctgc cccccaaac 1200

ccccctcctg cg

<210> 10

<211> 1212

<212> DNA

<213> Pan troglodytes

<400> 10

atgagtgact ccaaggaacc aagactgcag cagctgggcc tcctggagga ggaacagctg 60

agaggccttg gattccgaca gactcgaggc tacaagagct tagcagggtg tcttggccat 120

ggtcccctgg tgctgcaact cctctccttc acgctcttgg ctgggctcct tgtccaagtg 180

tccaaggtcc ccagctccat aagtcaggaa gaatccaggc aagacgtgat ctaccagaac 240

ctgaccacagc ttaaagctgc agtgggtgag ctctcagaga aatccaagct gcaggagatc 300

taccaggagc tgaccagct gaaggctgca gtgggtgagc ttccagagaa atctaagcag 360

caggagatct accaggagct gaccggctg aaggctgcag tgggtgagct tccagagaaa 420

tctaagatgc aggagatcta ccaggagctg actcggctga aggctgcagt gggtgagctt 480

ccagagaaat ctaagatgca ggagatctac caggagctga ctcggtgaa ggctgcagtg 540

ggtgagcttc cagagaaatc taagcagcag gagatctacc aggagctgac ccagctgaag 600

gctgcagtgg gtgagcttcc agagaaatct aagcagcagg agatctacca ggagctgacc 660

cagctgaagg ctgcagtggg tgagcttcca gagaaatcta agcagcagga gatctaccag 720
gagctgaccc ggctgaaggc tgcagtggaa cgctgtgcc gccgctgcc ctgggaatgg 780
acattcttcc aaggaaactg ttacttcatg tctaactccc agcggaactg gcaagactcc 840
atcactgcct gcaaagaagt gggggcccag ctgctgtaa tcaaaagtgc tgaggagcag 900
aatttcctac agctgcagtc ttccagaagt aaccgcttca cctggatggg actttcagat 960
ctaaatgagg aaggcatgtg gcaatgggtg gacggctcac ctctgttgcc cagcttcaac 1020
cagtaytggg acagaggaga gccaacaac gttggggagg aagactgcgc ggaatttagt 1080
ggcaatggct ggaatgacga caaatgtaat cttgccaaat tctggatctg caaaaagtcc 1140
gcagctcct gctccagga tgaagaacag tttctttctc cagcccctgc cccccaaac 1200
ccccctcctg cg 1212

<210> 11

<211> 1212

<212> DNA

<213> Gorilla gorilla

<400> 11

atgagtgact ccaaggaacc aagactgcag cagctgggcc tcttgaggga ggaacagctg 60

agaggccttg gattccgaca gactcgaggc tacaagagct tagcaggggtg tcttgccat 120

ggccccctgg tgctgcaact cctctccttc acgctcttgg ctgcgctcct tgtccaagtg 180

tccaaggtcc ccagctccat aagtcaggaa caatccaggc aagacgcgat ctaccagaac 240

ctgacctagt ttaaagctgc agtgggtgag ctctcagaga aatccaagct gcaggagatc 300

tatcaggagc tgacctagct gaaggctgca gtgggtgagc ttccagagaa atctaagcag 360

caggagatct accaggagct gagccagctg aaggctgcag tgggtgagct tccagagaaa 420

tctaagcagc aggagatcta ccaggagctg acccggtgta aggctgcagt ggggtgagctt 480

ccagagaaat ctaagcagca ggagatctac caggagctga cccggctgaa ggctgcagtg 540

ggtgagcttc cagagaaatc taagcagcag gagatctacc aggagctgag ccagctgaag 600

gctgcagtgg gtgagcttcc agagaaatct aagcagcagg agatctacca ggagctgagc 660

cagctgaagg ctgcagtggg tgagcttcca gagaaatcta agcagcagga gatctaccag 720

gagctgacct agctgaaggc tgcagtggaa cgctgtgcc gccgctgccc ctgggaatgg 780

acattcttcc aaggaaactg ttacttcatg tctaactccc agcggaactg gcacgactcc 840

atcaccgcct gccagaagt gggggcccag ctgcgtcgtta tcaaaagtgc tgaggagcag 900

aacttcttac agctgcagtc ttccagaagt aaccgcttca cctggatggg actttcagat 960

ctaaatcatg aaggcacgtg gcaatgggtg gacggctcac ctctgttgcc cagcttcgag 1020

cagtattgga acagaggaga gcccacaac gttggggagg aagactgcg ggaatttagt 1080

ggcaatggct ggaacgatga caaatgtaat cttgccaaat tctggatctg caaaaagtct 1140

gcagcctcct gctccaggga tgaagaacag tttctttctc cagcctctgc caccctctgc 1200

ccccctcctg cg 1212

<210> 12

<211> 105

<212> PRT

<213> Pan troglodytes

<400> 12

Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr

1 5 10 15

Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala

20 25 30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe

35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys

50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly

65 70 75 80

Thr Ser Leu Ser Glu Lys Thr Val Leu Leu Leu Val Thr Pro Phe Leu

85

90

95

Ala Ala Ala Ala Trp Ser Leu His Pro

100

105

<210> 13

<211> 121

<212> PRT

<213> Pan troglodytes

<400> 13

Ser Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr

1

5

10

15

Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala

20

25

30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Leu Glu His Cys Asn Phe

35

40

45

Lys Asp Leu Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys

50

55

60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly

65

70

75

80

Asn Glu Gln Leu Glu Asn Gly Gly Asn Glu Gln Leu Glu Asn Gly Gly

85

90

95

Thr Ser Leu Ser Glu Lys Thr Val Leu Leu Arg Val Thr Pro Phe Leu

100

105

110

Ala Ala Ala Ala Trp Ser Leu His Pro

115

120

<210> 14

<211> 5140

<212> DNA

<213> Homo sapiens

<400> 14

ctccagacct acccagaaag atgcccgat ggatcctgca gctccgtggc ttttctggga 60

agcagcggcc cctgctctca agagaccctg gctcctgatg gtggcccaa ggttgccagc 120

tgggtgctagg gactcaggac agtttcccag aaaaggccaa gcgggcagcc cctccagggg 180

ccgggtgagg aagctggggg gtgcggaggc cacactgggt ccctgaacct cctgcttggg 240

tacagtgcag ctctcaagt ccacagacgt gggccggcac agcctcctgt acctgaagga 300

aatcggccgt ggctgggtcg ggaagggtgt cctgggggag gtgaactctg gcatcagcag 360

tgccaggtg gtggtgaagg agctgcaggc tagtgccagc gtgcaggagc agatgcagtt 420

cctggaggag gtgcagccct acagggccct gaagcacagc aacctgctcc agtgcctggc 480

ccagtgcgcc gaggtgacgc cctacctgct ggtgatggag ttctgccac tgggggacct 540

caagggctac ctgcggagct gccgggtggc ggagtccatg gctcccgacc cccggaccct 600

gcagcgcatg gcctgtgagg tggcctgtgg cgtcctgcac cttcatcgca acaatttcgt 660

gcacagcgac ctggccctgc ggaactgcct gctcacggct gacctgacgg tgaagattgg 720

tgactatggc ctggctcact gcaagtacag agaggactac ttcgtgactg ccgaccagct 780

gtgggtgcct ctgcgctgga tcgcgccaga gctgggtggac gaggtgcata gcaacctgct 840

cgtcgtggac cagaccaaga gcgggaatgt gtgggtccctg ggcgtgacca tctgggagct 900

ctttgagctg ggcacgcagc cctatcccca gcactcggac cagcaggtgc tggcgtacac 960

ggtcggggag cagcagctca agctgccc aa gcccagctg cagctgaccc tgtcggaccg 1020

ctggtacgag gtgatgcagt tctgctggct gcagcccag cagcggccca cagccgagga 1080

ggtgcacctg ctgctgtcct acctgtgtgc caagggcgcc accgaagcag aggaggagtt 1140

tgaacggcgc tggcgtctc tgcggcccgg cgggggcggc gtggggcccg ggcccgggtc 1200

ggcggggccc atgctgggcg gcgtggtgga gctcgccgct gcctcgtcct tcccgtgct 1260

ggagcagttc gcgggcgacg gcttccacgc ggacggcgac gacgtgctga cggtgaccga 1320

gaccagccga ggcctcaatt ttgagtacaa gtgggaggcg ggccgcggcg cggaggcctt 1380

cccggccacg ctgagccctg gccgcaccgc acgctgcag gagctgtgcg cccccgacgg 1440

cgcgccccg ggcgtggttc cgggtgctcag cgcgcacagc ccgtcgctgg gcagcgagta 1500

cttcatccgc ctagaggagg ccgcacccgc cgccggccac gaccctgact gcgcgggctg 1560

cgccccagt ccacctgcca ccgcggacca ggacgacgac tctgacggca gcaccgccgc 1620

ctcgctggcc atggagccgc tgctgggcca cgggccaccc gtcgacgtcc cctggggccg 1680

cggcgaccac taccctcgca gaagcttggc gcgggacccg ctctgccctt cacgtctctc 1740

ctcgccctcg gcggggcccc tgagtctggc ggaggaggga gcggaggatg cagactgggg 1800

cgtggccgcc ttctgtcctg ctttcttcga ggaccactg ggcacgtccc ctttggggag 1860

ctcaggggcg ccccgctgc cgtgactgg cgaggatgag ctagaggagg tgggagcgcg 1920

gagggccgcc cagcgcgggc actggcgctc caacgtgtca gccacaaca acagcggcag 1980

ccgtgtcca gagtctggg acccgtctc tcggggctgc cagctgagg gctgccccag 2040

tccaaagcag acccacggg cctccccga gccgggtac cctggagagc ctctgcttgg 2100

gtccaggca gcctctgcc aggagccagg ctgctgccc gccctccctc atctatgctc 2160

tgccagggc ctggcacctg ctccctgctt ggttacacc tctggacag agacagccag 2220

tagtgggggt gaccaccgc aggcagagcc caagcttgcc acggaggctg agggcactac 2280

cggacccgc ctgcccctt cttcgtccc ctcccatcc caggaggag cccacttcc 2340

ctcggaggag gccagtgcc ccgacgccc tgatgccctg cctgactctc ccacgctgc 2400

tactggtggc gaggtgtctg ccatcaagct ggcttctgcc ctgaatggca gcagcagctc 2460

tcccgaggtg gaggcaccca gcagtgagga tgaggacacg gctgaggcca cctcaggcat 2520

cttcaccgac acgtccagcg acggcctgca ggccaggagg ccg gatgtgg tgccagcctt 2580

ccgctctctg cagaagcagg tggggacccc cgactccctg gactccctgg acatcccgtc 2640

ctcagccagt gatggtggct atgaggtctt cagcccgtcg gccactggcc cctctggagg 2700

gcagccgcga gcgctggaca gtggctatga caccgagaac tatgagtccc ctgagtttgt 2760

gctcaaggag gcgcaggaag ggtgtgagcc ccaggccttt gcggagctgg cctcagaggg 2820

tgagggcccc gggcccgaga cacggctctc cacctccctc agtggcctca acgagaagaa 2880

tccctaccga gactctgcct acttctcaga cctcagggtt gaggccgagg ccacctcagg 2940

cccagagaag aagtgcggcg gggaccgagc ccccgggcca gagctgggccc tgccgagcac 3000

tgggcagccg tctgagcagg tctgtctcag gcttgggggtt tccggggagg cacaaggctc 3060

tggccccggg gaggtgctgc cccactgct gcagcttgaa gggtcctccc cagagcccag 3120

cacctgcccc tcgggcctgg tcccagagcc tccggagccc caaggcccag ccaaggtgcg 3180

gcctgggccc agccccagct gctcccagtt tttctgctg accccggttc cgctgagatc 3240

agaaggcaac agctctgagt tccaggggcc ccaggactg ttgtcagggc cggccccaca 3300

aaagcggatg gggggcccag gcacccccag agcccactc cgcttggtc tgcccggcct 3360

ccctgcggcc ttggagggcc ggccggagga ggaggaggag gacagtgagg acagcgacga 3420

gtctgacgag gagctccgt gctacagcgt ccaggagcct agcgaggaca gcgaagagga 3480

ggcgccggcg gtgcccgtgg tggtaggtga gagccagagc gcgcgcaacc tgcgcagcct 3540

gctcaagatg cccagcctgc tgtccgagac cttctgcgag gacctggaac gcaagaagaa 3600

ggcgtgtcc ttcttcgacg acgtcacctg ctacctctt gaccaggaaa gcccacccg 3660

ggagctcggg gagcccttcc cgggcgcaa ggaatcgccc cctacgttcc ttagggggag 3720

ccccggctct cccagcgccc ccaaccggcc gcagcaggct gatgggtccc caaatggctc 3780

cacagcgga gaggggtggt ggttcgctg ggacgacgac ttcccgtga tgacggccaa 3840

ggcagccttc gccatggccc tagaccggc cgcacccgcc ccggtgcgc ccacgcccac 3900

gcccgtccc ttctgcgct tcacggtgtc gcccgcgccc acgtcccgt tctccatcac 3960

gcacgtgtct gactcgacg ccgagtcaa gagaggacct gaagctggtg ccgggggtga 4020

gagtaaagag gcttgagacc tgggcagctc ctgcccctca aggctggcgt caccggagcc 4080

cctgccaggc agcagcgagg atggtgaccg agaaggtggg gaccacgtcc tggtaggtgt 4140

tggcagcaga ttcaggtgcc tctgccccac gcggtgtcct ggagaagccc gtgggatgag 4200

aggccctgga tggtagatcg gccatgctcc gccccagagg cagaattcgt ctgggctttt 4260

aggcttgctg ctagcccctg ggggcgcctg gagccacagt ggggtgtctgt acacacatac 4320

acactcaaaa ggggccagtg cccctgggca cgggggcccc caccctctgc cctgcctgcc 4380

tggcctcgga ggaccgcgat gcccacatccg gcagctcctc cggtgtgctc acaggacact 4440

taaaccagga cgaggcatgg ccccgagaca ctggcaggtt tgtgagcctc ttcccacccc 4500

ctgtgcccc acccttgccct ggttcctggt ggctcagggc aaggagtggc cctgggcgcc 4560

cgtgtcggtc ctgtttccgc tgcccttata tcaaagtccg tggctgtttc cccttcactg 4620

actcagctag acccgtaagc ccacccttcc cacagggaac aggctgctcc cacctgggtc 4680

ccgctgtggc cacgggtggc agcccaaaag atcaggggtg gaggggcttc caggctgtac 4740

tcctgccccg tgggccccgt tctagaggtg cccttggcag gaccgtgcag gcagctcccc 4800

tctgtggggc agtatctggt cctgtgcccc agctgccaaa ggagagtggg ggccatgccc 4860

cgcagtcagt gttggggggc tcctgcctac agggagaggg atgggtggga aggggtggag 4920

ctgggggcag ggcagcacag ggaatatattt tgtaactaac taactgctgt ggttggagcg 4980

aatggaagtt gggtgatattt aagttattgt tgccaaagag atgtaaagtt tattgttgct 5040

tcgcaggggg atttgttttg tgttttgttt gaggcctaga acgctggtgc aatgttttct 5100

tggtccttgt tttttaagag aaatgaagct aagaaaaaag

5140

<210> 15

<211> 5140

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (413)..(4036)

<400> 15

ctccagacct acccagaaag atgcccggat ggatcctgca gctccgtggc ttttctggga 60

agcagcggcc cctgctctca agagaccctg gctcctgatg gtggcccaa ggttgccagc 120

tggtgctagg gactcaggac agtttcccag aaaaggccaa gcgggcagcc cctccagggg 180

ccgggtgagg aagctggggg gtgcggaggc cacactgggt ccctgaacc cctgcttggt 240

tacagtgcag ctctcaagt ccacagacgt gggccggcac agcctcctgt acctgaagga 300

aatcgccgt ggctgggtcg ggaaggtgtt cctgggggag gtgaactctg gcatcagcag 360

tgcccaggtg gtggtgaagg agctgcaggc tagtgccagc gtgcaggagc ag atg cag 418

Met Gln

1

ttc ctg gag gag gtg cag ccc tac agg gcc ctg aag cac agc aac ctg 466

Phe Leu Glu Glu Val Gln Pro Tyr Arg Ala Leu Lys His Ser Asn Leu

5

10

15

ctc cag tgc ctg gcc cag tgc gcc gag gtg acg ccc tac ctg ctg gtg 514

Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro Tyr Leu Leu Val

20

25

30

atg gag ttc tgc cca ctg ggg gac ctc aag ggc tac ctg cgg agc tgc 562

Met Glu Phe Cys Pro Leu Gly Asp Leu Lys Gly Tyr Leu Arg Ser Cys

35

40

45

50

cgg gtg gcg gag tcc atg gct ccc gac ccc cgg acc ctg cag cgc atg 610

Arg Val Ala Glu Ser Met Ala Pro Asp Pro Arg Thr Leu Gln Arg Met

55

60

65

gcc tgt gag gtg gcc tgt ggc gtc ctg cac ctt cat cgc aac aat ttc 658

Ala Cys Glu Val Ala Cys Gly Val Leu His Leu His Arg Asn Asn Phe

70

75

80

gtg cac agc gac ctg gcc ctg cgg aac tgc ctg ctc acg gct gac ctg 706

Val His Ser Asp Leu Ala Leu Arg Asn Cys Leu Leu Thr Ala Asp Leu

85

90

95

acg gtg aag att ggt gac tat ggc ctg gct cac tgc aag tac aga gag 754

Thr Val Lys Ile Gly Asp Tyr Gly Leu Ala His Cys Lys Tyr Arg Glu

100

105

110

gac tac ttc gtg act gcc gac cag ctg tgg gtg cct ctg cgc tgg atc 802

Asp Tyr Phe Val Thr Ala Asp Gln Leu Trp Val Pro Leu Arg Trp Ile

115

120

125

130

gcg cca gag ctg gtg gac gag gtg cat agc aac ctg ctc gtc gtg gac	850
Ala Pro Glu Leu Val Asp Glu Val His Ser Asn Leu Leu Val Val Asp	
135 140 145	
cag acc aag agc ggg aat gtg tgg tcc ctg ggc gtg acc atc tgg gag	898
Gln Thr Lys Ser Gly Asn Val Trp Ser Leu Gly Val Thr Ile Trp Glu	
150 155 160	
ctc ttt gag ctg ggc acg cag ccc tat ccc cag cac tcg gac cag cag	946
Leu Phe Glu Leu Gly Thr Gln Pro Tyr Pro Gln His Ser Asp Gln Gln	
165 170 175	
gtg ctg gcg tac acg gtc cgg gag cag cag ctc aag ctg ccc aag ccc	994
Val Leu Ala Tyr Thr Val Arg Glu Gln Gln Leu Lys Leu Pro Lys Pro	
180 185 190	
cag ctg cag ctg acc ctg tcg gac cgc tgg tac gag gtg atg cag ttc	1042
Gln Leu Gln Leu Thr Leu Ser Asp Arg Trp Tyr Glu Val Met Gln Phe	
195 200 205 210	
tgc tgg ctg cag ccc gag cag cgg ccc aca gcc gag gag gtg cac ctg	1090
Cys Trp Leu Gln Pro Glu Gln Arg Pro Thr Ala Glu Glu Val His Leu	
215 220 225	
ctg ctg tcc tac ctg tgt gcc aag ggc gcc acc gaa gca gag gag gag	1138
Leu Leu Ser Tyr Leu Cys Ala Lys Gly Ala Thr Glu Ala Glu Glu Glu	
230 235 240	
ttt gaa cgg cgc tgg cgc tct ctg cgg ccc ggc ggg ggc ggc gtg ggg	1186
Phe Glu Arg Arg Trp Arg Ser Leu Arg Pro Gly Gly Gly Gly Val Gly	
245 250 255	

ccc ggg ccc ggt gcg gcg ggg ccc atg ctg ggc ggc gtg gtg gag ctc 1234
 Pro Gly Pro Gly Ala Ala Gly Pro Met Leu Gly Gly Val Val Glu Leu

260

265

270

gcc gct gcc tcg tcc ttc ccg ctg ctg gag cag ttc gcg ggc gac ggc 1282
 Ala Ala Ala Ser Ser Phe Pro Leu Leu Glu Gln Phe Ala Gly Asp Gly

275

280

285

290

ttc cac gcg gac ggc gac gac gtg ctg acg gtg acc gag acc agc cga 1330
 Phe His Ala Asp Gly Asp Asp Val Leu Thr Val Thr Glu Thr Ser Arg

295

300

305

ggc ctc aat ttt gag tac aag tgg gag gcg ggc cgc ggc gcg gag gcc 1378
 Gly Leu Asn Phe Glu Tyr Lys Trp Glu Ala Gly Arg Gly Ala Glu Ala

310

315

320

ttc ccg gcc acg ctg agc cct ggc cgc acc gca cgc ctg cag gag ctg 1426
 Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln Glu Leu

325

330

335

tgc gcc ccc gac ggc gcg ccc ccg ggc gtg gtt ccg gtg ctc agc gcg 1474
 Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu Ser Ala

340

345

350

cac agc ccg tcg ctg ggc agc gag tac ttc atc cgc cta gag gag gcc 1522
 His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu Glu Ala

355

360

365

370

gca ccc gcc gcc ggc cac gac cct gac tgc gcc ggc tgc gcc ccc agt 1570

Ala Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala Pro Ser	
375 380 385	
cca cct gcc acc gcg gac cag gac gac gac tct gac ggc agc acc gcc	1618
Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser Thr Ala	
390 395 400	
gcc tcg ctg gcc atg gag ccg ctg ctg ggc cac ggg cca ccc gtc gac	1666
Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Gly Pro Pro Val Asp	
405 410 415	
gtc ccc tgg ggc cgc ggc gac cac tac cct cgc aga agc ttg gcg cgg	1714
Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu Ala Arg	
420 425 430	
gac ccg ctc tgc ccc tca cgc tct ccc tcg ccc tcg gcg ggc ccc ctg	1762
Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly Pro Leu	
435 440 445 450	
agt ctg gcg gag gga gga gcg gag gat gca gac tgg ggc gtg gcc gcc	1810
Ser Leu Ala Glu Gly Gly Ala Glu Asp Ala Asp Trp Gly Val Ala Ala	
455 460 465	
ttc tgt cct gcc ttc ttc gag gac cca ctg ggc acg tcc cct ttg ggg	1858
Phe Cys Pro Ala Phe Phe Glu Asp Pro Leu Gly Thr Ser Pro Leu Gly	
470 475 480	
agc tca ggg gcg ccc ccg ctg ccg ctg act ggc gag gat gag cta gag	1906
Ser Ser Gly Ala Pro Pro Leu Pro Leu Thr Gly Glu Asp Glu Leu Glu	
485 490 495	

gag gtg gga gcg cgg agg gcc gcc cag cgc ggg cac tgg cgc tcc aac	1954
Glu Val Gly Ala Arg Arg Ala Ala Gln Arg Gly His Trp Arg Ser Asn	
500 505 510	
gtg tca gcc aac aac aac agc ggc agc cgc tgt cca gag tcc tgg gac	2002
Val Ser Ala Asn Asn Asn Ser Gly Ser Arg Cys Pro Glu Ser Trp Asp	
515 520 525 530	
ccc gtc tct gcg ggc tgc cac gct gag ggc tgc ccc agt cca aag cag	2050
Pro Val Ser Ala Gly Cys His Ala Glu Gly Cys Pro Ser Pro Lys Gln	
535 540 545	
acc cca cgg gcc tcc ccc gag ccg ggg tac cct gga gag cct ctg ctt	2098
Thr Pro Arg Ala Ser Pro Glu Pro Gly Tyr Pro Gly Glu Pro Leu Leu	
550 555 560	
ggg ctc cag gca gcc tct gcc cag gag cca ggc tgc tgc ccc ggc ctc	2146
Gly Leu Gln Ala Ala Ser Ala Gln Glu Pro Gly Cys Cys Pro Gly Leu	
565 570 575	
cct cat cta tgc tct gcc cag ggc ctg gca cct gct ccc tgc ctg gtt	2194
Pro His Leu Cys Ser Ala Gln Gly Leu Ala Pro Ala Pro Cys Leu Val	
580 585 590	
aca ccc tcc tgg aca gag aca gcc agt agt ggg ggt gac cac ccg cag	2242
Thr Pro Ser Trp Thr Glu Thr Ala Ser Ser Gly Gly Asp His Pro Gln	
595 600 605 610	
gca gag ccc aag ctt gcc acg gag gct gag ggc act acc gga ccc cgc	2290
Ala Glu Pro Lys Leu Ala Thr Glu Ala Glu Gly Thr Thr Gly Pro Arg	

615	620	625	
ctg ccc ctt cct tcc gtc ccc tcc cca tcc cag gag gga gcc cca ctt			2338
Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Gln Glu Gly Ala Pro Leu			
630	635	640	
ccc tcg gag gag gcc agt gcc ccc gac gcc cct gat gcc ctg cct gac			2386
Pro Ser Glu Glu Ala Ser Ala Pro Asp Ala Pro Asp Ala Leu Pro Asp			
645	650	655	
tct ccc acg cct gct act ggt ggc gag gtg tct gcc atc aag ctg gct			2434
Ser Pro Thr Pro Ala Thr Gly Gly Glu Val Ser Ala Ile Lys Leu Ala			
660	665	670	
tct gcc ctg aat ggc agc agc agc tct ccc gag gtg gag gca ccc agc			2482
Ser Ala Leu Asn Gly Ser Ser Ser Ser Pro Glu Val Glu Ala Pro Ser			
675	680	685	690
agt gag gat gag gac acg gct gag gcc acc tca ggc atc ttc acc gac			2530
Ser Glu Asp Glu Asp Thr Ala Glu Ala Thr Ser Gly Ile Phe Thr Asp			
695	700	705	
acg tcc agc gac ggc ctg cag gcc agg agg ccg gat gtg gtg cca gcc			2578
Thr Ser Ser Asp Gly Leu Gln Ala Arg Arg Pro Asp Val Val Pro Ala			
710	715	720	
ttc cgc tct ctg cag aag cag gtg ggg acc ccc gac tcc ctg gac tcc			2626
Phe Arg Ser Leu Gln Lys Gln Val Gly Thr Pro Asp Ser Leu Asp Ser			
725	730	735	
ctg gac atc ccg tcc tca gcc agt gat ggt ggc tat gag gtc ttc agc			2674

Leu Asp Ile Pro Ser Ser Ala Ser Asp Gly Gly Tyr Glu Val Phe Ser

740

745

750

ccg tcg gcc act ggc ccc tct gga ggg cag ccg cga gcg ctg gac agt 2722

Pro Ser Ala Thr Gly Pro Ser Gly Gly Gln Pro Arg Ala Leu Asp Ser

755

760

765

770

ggc tat gac acc gag aac tat gag tcc cct gag ttt gtg ctc aag gag 2770

Gly Tyr Asp Thr Glu Asn Tyr Glu Ser Pro Glu Phe Val Leu Lys Glu

775

780

785

gcg cag gaa ggg tgt gag ccc cag gcc ttt gcg gag ctg gcc tca gag 2818

Ala Gln Glu Gly Cys Glu Pro Gln Ala Phe Ala Glu Leu Ala Ser Glu

790

795

800

ggt gag ggc ccc ggg ccc gag aca cgg ctc tcc acc tcc ctc agt ggc 2866

Gly Glu Gly Pro Gly Pro Glu Thr Arg Leu Ser Thr Ser Leu Ser Gly

805

810

815

ctc aac gag aag aat ccc tac cga gac tct gcc tac ttc tca gac ctc 2914

Leu Asn Glu Lys Asn Pro Tyr Arg Asp Ser Ala Tyr Phe Ser Asp Leu

820

825

830

gag gct gag gcc gag gcc acc tca ggc cca gag aag aag tgc ggc ggg 2962

Glu Ala Glu Ala Glu Ala Thr Ser Gly Pro Glu Lys Lys Cys Gly Gly

835

840

845

850

gac cga gcc ccc ggg cca gag ctg ggc ctg ccg agc act ggg cag ccg 3010

Asp Arg Ala Pro Gly Pro Glu Leu Gly Leu Pro Ser Thr Gly Gln Pro

855

860

865

tct gag cag gtc tgt ctc agg cct ggg gtt tcc ggg gag gca caa ggc	3058
Ser Glu Gln Val Cys Leu Arg Pro Gly Val Ser Gly Glu Ala Gln Gly	
870 875 880	
tct ggc ccc ggg gag gtg ctg ccc cca ctg ctg cag ctt gaa ggg tcc	3106
Ser Gly Pro Gly Glu Val Leu Pro Pro Leu Leu Gln Leu Glu Gly Ser	
885 890 895	
tcc cca gag ccc agc acc tgc ccc tcg ggc ctg gtc cca gag cct ccg	3154
Ser Pro Glu Pro Ser Thr Cys Pro Ser Gly Leu Val Pro Glu Pro Pro	
900 905 910	
gag ccc caa ggc cca gcc aag gtg cgg cct ggg ccc agc ccc agc tgc	3202
Glu Pro Gln Gly Pro Ala Lys Val Arg Pro Gly Pro Ser Pro Ser Cys	
915 920 925 930	
tcc cag ttt ttc ctg ctg acc ccg gtt ccg ctg aga tca gaa ggc aac	3250
Ser Gln Phe Phe Leu Leu Thr Pro Val Pro Leu Arg Ser Glu Gly Asn	
935 940 945	
agc tct gag ttc cag ggg ccc cca gga ctg ttg tca ggg ccg gcc cca	3298
Ser Ser Glu Phe Gln Gly Pro Pro Gly Leu Leu Ser Gly Pro Ala Pro	
950 955 960	
caa aag cgg atg ggg ggc cca ggc acc ccc aga gcc cca ctc cgc ctg	3346
Gln Lys Arg Met Gly Gly Pro Gly Thr Pro Arg Ala Pro Leu Arg Leu	
965 970 975	
gct ctg ccc ggc ctc cct gcg gcc ttg gag ggc cgg ccg gag gag gag	3394
Ala Leu Pro Gly Leu Pro Ala Ala Leu Glu Gly Arg Pro Glu Glu Glu	

980

985

990

gag gag gac agt gag gac agc gac gag tct gac gag gag ctc cgc tgc 3442

Glu Glu Asp Ser Glu Asp Ser Asp Glu Ser Asp Glu Glu Leu Arg Cys

995

1000

1005

1010

tac agc gtc cag gag cct agc gag gac agc gaa gag gag gcg ccg gcg 3490

Tyr Ser Val Gln Glu Pro Ser Glu Asp Ser Glu Glu Glu Ala Pro Ala

1015

1020

1025

gtg ccc gtg gtg gtg gct gag agc cag agc gcg cgc aac ctg cgc agc 3538

Val Pro Val Val Val Ala Glu Ser Gln Ser Ala Arg Asn Leu Arg Ser

1030

1035

1040

ctg ctc aag atg ccc agc ctg ctg tcc gag acc ttc tgc gag gac ctg 3586

Leu Leu Lys Met Pro Ser Leu Leu Ser Glu Thr Phe Cys Glu Asp Leu

1045

1050

1055

gaa cgc aag aag aag gcc gtg tcc ttc ttc gac gac gtc acc gtc tac 3634

Glu Arg Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr Val Tyr

1060

1065

1070

ctc ttt gac cag gaa agc ccc acc cgg gag ctc ggg gag ccc ttc ccg 3682

Leu Phe Asp Gln Glu Ser Pro Thr Arg Glu Leu Gly Glu Pro Phe Pro

1075

1080

1085

1090

ggc gcc aag gaa tcg ccc cct acg ttc ctt agg ggg agc ccc ggc tct 3730

Gly Ala Lys Glu Ser Pro Pro Thr Phe Leu Arg Gly Ser Pro Gly Ser

1095

1100

1105

ccc agc gcc ccc aac cgg ccg cag cag gct gat ggc tcc cca aat ggc 3778

Pro Ser Ala Pro Asn Arg Pro Gln Gln Ala Asp Gly Ser Pro Asn Gly

1110

1115

1120

tcc aca gcg gaa gag ggt ggt ggg ttc gcg tgg gac gac gac ttc ccg 3826

Ser Thr Ala Glu Glu Gly Gly Gly Phe Ala Trp Asp Asp Asp Phe Pro

1125

1130

1135

ctg atg acg gcc aag gca gcc ttc gcc atg gcc cta gac ccg gcc gca 3874

Leu Met Thr Ala Lys Ala Ala Phe Ala Met Ala Leu Asp Pro Ala Ala

1140

1145

1150

ccc gcc ccg gct gcg ccc acg ccc acg ccc gct ccc ttc tcg cgc ttc 3922

Pro Ala Pro Ala Ala Pro Thr Pro Thr Pro Ala Pro Phe Ser Arg Phe

1155

1160

1165

1170

acg gtg tcg ccc gcg ccc acg tcc cgc ttc tcc atc acg cac gtg tct 3970

Thr Val Ser Pro Ala Pro Thr Ser Arg Phe Ser Ile Thr His Val Ser

1175

1180

1185

gac tcg gac gcc gag tcc aag aga gga cct gaa gct ggt gcc ggg ggt 4018

Asp Ser Asp Ala Glu Ser Lys Arg Gly Pro Glu Ala Gly Ala Gly Gly

1190

1195

1200

gag agt aaa gag gct tga gacctgggca gctcctgccc ctcaaggctg 4066

Glu Ser Lys Glu Ala

1205

gcgtcaccgg agcccctgcc aggcagcagc gaggatggtg accgagaagg tggggaccac 4126

gtcctggtgg ctgttggcag cagattcagg tgcctctgcc ccacgcggtg tcctggagaa 4186

gcccgtggga tgagaggccc tggatggtag atcgccatg ctccgcccc gaggcagaat 4246

tcgtctgggc ttttaggctt gctgctagcc cctgggggcg cctggagcca cagtgggtgt 4306

ctgtacacac atacacactc aaaagggggc agtgcccctg ggcacggcgg cccccaccct 4366

ctgccctgcc tgccctggcct cggaggaccc gcatgcccc tccggcagct cctccggtgt 4426

gctcacagga cacttaaacc aggacgaggc atggccccga gacactggca ggtttgtgag 4486

cctcttcca cccctgtgc cccaccctt gcctgggtcc tggaggctca gggcaaggag 4546

tgccctggg cgccctgtc ggtcctgtt ccgtgccct tatctcaaag tccgtggctg 4606

ttccccctc actgactcag ctagaccgt aagcccacc tttccacagg gaacaggctg 4666

ctccacctg ggtcccgtg tggccacggt gggcagcca aaagatcagg ggtggagggg 4726

ctccaggct gtactcctgc cccgtgggccc ccgttctaga ggtgcccttg gcaggaccgt 4786

gcaggcagct cccctctgtg gggcagtatc tggctcctgt cccagctgc caaaggagag 4846

tgggggcat gcccgcagt cagtgttggg gggctcctgc ctacaggag agggatggtg 4906

gggaaggggt ggagctgggg gcagggcagc acagggaata tttttgtaac taactaactg 4966

ctgtggttgg agcgaatgga agttgggtga ttttaagtta ttgttgcaa agagatgtaa 5026

agtttattgt tgcttcgcag ggggatttgt tttgtgttt gtttgaggct tagaacgctg 5086

gtgcaatgtt ttcttggtcc ttgtttttta agagaaatga agctaagaaa aaag 5140

<210> 16

<211> 1207

<212> PRT

<213> Homo sapiens

<400> 16

Met Gln Phe Leu Glu Glu Val Gln Pro Tyr Arg Ala Leu Lys His Ser
1 5 10 15

Asn Leu Leu Gln Cys Leu Ala Gln Cys Ala Glu Val Thr Pro Tyr Leu
20 25 30

Leu Val Met Glu Phe Cys Pro Leu Gly Asp Leu Lys Gly Tyr Leu Arg
35 40 45

Ser Cys Arg Val Ala Glu Ser Met Ala Pro Asp Pro Arg Thr Leu Gln
50 55 60

Arg Met Ala Cys Glu Val Ala Cys Gly Val Leu His Leu His Arg Asn
65 70 75 80

Asn Phe Val His Ser Asp Leu Ala Leu Arg Asn Cys Leu Leu Thr Ala
85 90 95

Asp Leu Thr Val Lys Ile Gly Asp Tyr Gly Leu Ala His Cys Lys Tyr
100 105 110

Arg	Glu	Asp	Tyr	Phe	Val	Thr	Ala	Asp	Gln	Leu	Trp	Val	Pro	Leu	Arg
		115						120						125	
Trp	Ile	Ala	Pro	Glu	Leu	Val	Asp	Glu	Val	His	Ser	Asn	Leu	Leu	Val
		130					135						140		
Val	Asp	Gln	Thr	Lys	Ser	Gly	Asn	Val	Trp	Ser	Leu	Gly	Val	Thr	Ile
145					150					155					160
Trp	Glu	Leu	Phe	Glu	Leu	Gly	Thr	Gln	Pro	Tyr	Pro	Gln	His	Ser	Asp
				165					170					175	
Gln	Gln	Val	Leu	Ala	Tyr	Thr	Val	Arg	Glu	Gln	Gln	Leu	Lys	Leu	Pro
			180					185					190		
Lys	Pro	Gln	Leu	Gln	Leu	Thr	Leu	Ser	Asp	Arg	Trp	Tyr	Glu	Val	Met
		195					200					205			
Gln	Phe	Cys	Trp	Leu	Gln	Pro	Glu	Gln	Arg	Pro	Thr	Ala	Glu	Glu	Val
		210				215						220			
His	Leu	Leu	Leu	Ser	Tyr	Leu	Cys	Ala	Lys	Gly	Ala	Thr	Glu	Ala	Glu
225					230					235				240	
Glu	Glu	Phe	Glu	Arg	Arg	Trp	Arg	Ser	Leu	Arg	Pro	Gly	Gly	Gly	Gly
				245					250					255	
Val	Gly	Pro	Gly	Pro	Gly	Ala	Ala	Gly	Pro	Met	Leu	Gly	Gly	Val	Val
			260					265						270	

Glu Leu Ala Ala Ala Ser Ser Phe Pro Leu Leu Glu Gln Phe Ala Gly

275

280

285

Asp Gly Phe His Ala Asp Gly Asp Asp Val Leu Thr Val Thr Glu Thr

290

295

300

Ser Arg Gly Leu Asn Phe Glu Tyr Lys Trp Glu Ala Gly Arg Gly Ala

305

310

315

320

Glu Ala Phe Pro Ala Thr Leu Ser Pro Gly Arg Thr Ala Arg Leu Gln

325

330

335

Glu Leu Cys Ala Pro Asp Gly Ala Pro Pro Gly Val Val Pro Val Leu

340

345

350

Ser Ala His Ser Pro Ser Leu Gly Ser Glu Tyr Phe Ile Arg Leu Glu

355

360

365

Glu Ala Ala Pro Ala Ala Gly His Asp Pro Asp Cys Ala Gly Cys Ala

370

375

380

Pro Ser Pro Pro Ala Thr Ala Asp Gln Asp Asp Asp Ser Asp Gly Ser

385

390

395

400

Thr Ala Ala Ser Leu Ala Met Glu Pro Leu Leu Gly His Gly Pro Pro

405

410

415

Val Asp Val Pro Trp Gly Arg Gly Asp His Tyr Pro Arg Arg Ser Leu

420

425

430

Ala Arg Asp Pro Leu Cys Pro Ser Arg Ser Pro Ser Pro Ser Ala Gly

435

440

445

Pro Leu Ser Leu Ala Glu Gly Gly Ala Glu Asp Ala Asp Trp Gly Val

450

455

460

Ala Ala Phe Cys Pro Ala Phe Phe Glu Asp Pro Leu Gly Thr Ser Pro

465

470

475

480

Leu Gly Ser Ser Gly Ala Pro Pro Leu Pro Leu Thr Gly Glu Asp Glu

485

490

495

Leu Glu Glu Val Gly Ala Arg Arg Ala Ala Gln Arg Gly His Trp Arg

500

505

510

Ser Asn Val Ser Ala Asn Asn Asn Ser Gly Ser Arg Cys Pro Glu Ser

515

520

525

Trp Asp Pro Val Ser Ala Gly Cys His Ala Glu Gly Cys Pro Ser Pro

530

535

540

Lys Gln Thr Pro Arg Ala Ser Pro Glu Pro Gly Tyr Pro Gly Glu Pro

545

550

555

560

Leu Leu Gly Leu Gln Ala Ala Ser Ala Gln Glu Pro Gly Cys Cys Pro

565

570

575

Gly Leu Pro His Leu Cys Ser Ala Gln Gly Leu Ala Pro Ala Pro Cys

580

585

590

Leu Val Thr Pro Ser Trp Thr Glu Thr Ala Ser Ser Gly Gly Asp His

595

600

605

Pro Gln Ala Glu Pro Lys Leu Ala Thr Glu Ala Glu Gly Thr Thr Gly
610 615 620

Pro Arg Leu Pro Leu Pro Ser Val Pro Ser Pro Ser Gln Glu Gly Ala
625 630 635 640

Pro Leu Pro Ser Glu Glu Ala Ser Ala Pro Asp Ala Pro Asp Ala Leu
645 650 655

Pro Asp Ser Pro Thr Pro Ala Thr Gly Gly Glu Val Ser Ala Ile Lys
660 665 670

Leu Ala Ser Ala Leu Asn Gly Ser Ser Ser Ser Pro Glu Val Glu Ala
675 680 685

Pro Ser Ser Glu Asp Glu Asp Thr Ala Glu Ala Thr Ser Gly Ile Phe
690 695 700

Thr Asp Thr Ser Ser Asp Gly Leu Gln Ala Arg Arg Pro Asp Val Val
705 710 715 720

Pro Ala Phe Arg Ser Leu Gln Lys Gln Val Gly Thr Pro Asp Ser Leu
725 730 735

Asp Ser Leu Asp Ile Pro Ser Ser Ala Ser Asp Gly Gly Tyr Glu Val
740 745 750

Phe Ser Pro Ser Ala Thr Gly Pro Ser Gly Gly Gln Pro Arg Ala Leu
755 760 765

Asp Ser Gly Tyr Asp Thr Glu Asn Tyr Glu Ser Pro Glu Phe Val Leu
770 775 780

Lys Glu Ala Gln Glu Gly Cys Glu Pro Gln Ala Phe Ala Glu Leu Ala
785 790 795 800

Ser Glu Gly Glu Gly Pro Gly Pro Glu Thr Arg Leu Ser Thr Ser Leu
805 810 815

Ser Gly Leu Asn Glu Lys Asn Pro Tyr Arg Asp Ser Ala Tyr Phe Ser
820 825 830

Asp Leu Glu Ala Glu Ala Glu Ala Thr Ser Gly Pro Glu Lys Lys Cys
835 840 845

Gly Gly Asp Arg Ala Pro Gly Pro Glu Leu Gly Leu Pro Ser Thr Gly
850 855 860

Gln Pro Ser Glu Gln Val Cys Leu Arg Pro Gly Val Ser Gly Glu Ala
865 870 875 880

Gln Gly Ser Gly Pro Gly Glu Val Leu Pro Pro Leu Leu Gln Leu Glu
885 890 895

Gly Ser Ser Pro Glu Pro Ser Thr Cys Pro Ser Gly Leu Val Pro Glu
900 905 910

Pro Pro Glu Pro Gln Gly Pro Ala Lys Val Arg Pro Gly Pro Ser Pro
915 920 925

Ser Cys Ser Gln Phe Phe Leu Leu Thr Pro Val Pro Leu Arg Ser Glu
930 935 940

Gly Asn Ser Ser Glu Phe Gln Gly Pro Pro Gly Leu Leu Ser Gly Pro
945 950 955 960

Ala Pro Gln Lys Arg Met Gly Gly Pro Gly Thr Pro Arg Ala Pro Leu
965 970 975

Arg Leu Ala Leu Pro Gly Leu Pro Ala Ala Leu Glu Gly Arg Pro Glu
980 985 990

Glu Glu Glu Glu Asp Ser Glu Asp Ser Asp Glu Ser Asp Glu Glu Leu
995 1000 1005

Arg Cys Tyr Ser Val Gln Glu Pro Ser Glu Asp Ser Glu Glu Glu Ala
1010 1015 1020

Pro Ala Val Pro Val Val Val Ala Glu Ser Gln Ser Ala Arg Asn Leu
1025 1030 1035 1040

Arg Ser Leu Leu Lys Met Pro Ser Leu Leu Ser Glu Thr Phe Cys Glu
1045 1050 1055

Asp Leu Glu Arg Lys Lys Lys Ala Val Ser Phe Phe Asp Asp Val Thr
1060 1065 1070

Val Tyr Leu Phe Asp Gln Glu Ser Pro Thr Arg Glu Leu Gly Glu Pro
1075 1080 1085

Phe Pro Gly Ala Lys Glu Ser Pro Pro Thr Phe Leu Arg Gly Ser Pro			
1090	1095	1100	
Gly Ser Pro Ser Ala Pro Asn Arg Pro Gln Gln Ala Asp Gly Ser Pro			
105	1110	1115	1120
Asn Gly Ser Thr Ala Glu Glu Gly Gly Gly Phe Ala Trp Asp Asp Asp			
	1125	1130	1135
Phe Pro Leu Met Thr Ala Lys Ala Ala Phe Ala Met Ala Leu Asp Pro			
1140	1145	1150	
Ala Ala Pro Ala Pro Ala Ala Pro Thr Pro Thr Pro Ala Pro Phe Ser			
1155	1160	1165	
Arg Phe Thr Val Ser Pro Ala Pro Thr Ser Arg Phe Ser Ile Thr His			
1170	1175	1180	
Val Ser Asp Ser Asp Ala Glu Ser Lys Arg Gly Pro Glu Ala Gly Ala			
1185	1190	1195	1200
Gly Gly Glu Ser Lys Glu Ala			
	1205		
<210> 17			
<211> 1803			
<212> DNA			
<213> Pan troglodytes			

<400> 17

gctccctgcc tggttacacc ctcttgaca gagacagccg gtagtggggg tgaccacccg 60

caggcagagc ccaagcttgc cacggaggct gagggcactg ccggaccctg tctgcccctt 120

ccttccgtcc cctccccatc ccaggaggga gcccacttc cctcggagga ggccagtgcc 180

cctgacgcc ctgatgcct gctgactct cccatgcctg ctactggtg cgaggtgtct 240

gccatcaagc tggcttctgt cctgaatggc agcagcagct ctcccaggt ggaggcacc 300

agcagcgagg atgaggacac ggctgaggcc acctcaggca tcttcaccga cacgtccagc 360

gacggcctgc aggccgagag gctggatgtg gtgccagcct tccgctctct gcagaagcag 420

gtggggaccc ccgactccct ggactccctg gacatcccat cctcagccag tgatggtggc 480

tatgaggtct tcagcccgtc ggccactggc ccctctggag ggagccccg agcgctggac 540

agtggctatg acaccgagaa ctatgagtc cctgagtttg tgctcaagga ggcgaggaa 600

gggtgtgagc ccaggcctt tgaggagctg gcctcagagg gtgaggggcc cgggccccggg 660

cccagacgc ggctctccac ctccctcagt ggcctcaacg agaagaatcc ctaccgagac 720

tctgcctact tctcagacct ggaggctgag gccgaggccg aggccacctc agggccagag 780

aagaagtgcg gcggggacca agccccggg ccagagctgg acctgccgag cactgggcag 840

ccgtctgagc aggtctccct caggcctggg gtttccgggg aggcacaagg ctctggcccc 900

ggggaggtgc tgccccact gctgcggctt gaaggatcct cccagagcc cagcacctgc 960

ccctcgggcc tgggccaga gcctccggag cccaaggcc cagccgaggt gcggcctggg 1020

cccagcccca gctgctcca gtttttctg ctgaccccg ttccgctgag atcagaaggc 1080

aacagctctg agttccagg gccccagga ctgttgtag ggccggcccc aaaaagcgg 1140

atggggggcc taggcacccc cagagcccca ctccgcctgg ctctgcccg cctccctgcg 1200

gccttgagg gccggccgga ggaggaggag gaggacagt aggacagcg cgagtctgac 1260

gaggagctcc gctgctacag cgtccaggag cctagcgagg acagcgaaga ggaggcgccg 1320

gcggtgcccg tgggtgtggc tgagagccag agcgcgcga acctgcgag cctgctcaag 1380

atgccagcc tgctgtccga ggccttctgc gaggacctg aacgcaaga gaaggccgtg 1440

tccttcttcg acgacgtcac cgtctacctc ttgaccagg aaagccccac ctgggagctc 1500

ggggagccct tcccgggccc caaggaatcg cccccacgt tccttagggg gagccccggc 1560

tctcccagcg ccccaaccg gccgcagcag gctgatggct ccccaaatgg ctccacagcg 1620

gaagaggggtg gtgggttcgc gtgggacgac gacttcccgc tgatgccggc caaggcagcc 1680

ttcgccatgg cctagaccc ggccgcaccc gcccggctg cgcacgcc cgtcccttc 1740

tcgcgcttca cgggtgtgcc cgcgcccacg tccacgtccc gttctccat cagcacgtg 1800

<210> 18

<211> 1785

<212> DNA

<213> Gorilla gorilla

<400> 18

gctccctgcc tggttacacc ctcttgaca gagacagacg gtagtggggg tgaccacccg 60

caggcagagc ccaagcttgc cacggaggct gagggcactg ccggaccccg cctgcccctt 120

ccttcggtcc cctccccatc ccaggaggga gcccacttc cctcggagga ggccagtgcc 180

cccgacgccc ctgatgcctt gcctgactcg ccacgcctg ctactggtgg cgaggtgtct 240

gccaccaagc tggcttccgc cctgaatggc agcagcagct ctcccaggt ggaggcaccc 300

agcagtgagg atgaggacac ggctgaggca acctcaggca tcttcaccga cacgtccagc 360

gacggcctgc aggccgagag gcaggatgtg gtgccagcct tccactctct gcagaagcag 420

gtggggaccc ccgactccct ggactccctg gacatcccgt cctcagccag tgatggtggc 480

tatgaggtct tcagcccgtc ggccacgggc ccctctggag ggcagccccc agcgtggac 540

agtggctatg acaccgagaa ctatgagtcc cctgagtttg tgctcaagga ggcgcaggaa 600

gggtgtgagc cccaggcctt tgcggagctg gcctcagagg gcgaggggcc cgggcccag 660

acgcggctct ccacctccct cagtggcctc aacgagaaga atccctaccg agattctgcc 720

tacttctcag acctggaggc tgaggccgag gctacctcag gcccagagaa gaagtgcggt 780

ggggaccaag cccccgggcc agagctgggc ctgccgagca ctgggcagcc gtctgagcag 840

gtctccctca gtccctggggt ttccgtggag gcacaaggct ctggccccgg ggaggtgctg 900

ccccactgc tgcggcttga agggctcctcc ccagagccca gcacctgcc ctcgggcctg 960

gtcccagagc ctccggagcc ccaaggccca gccgaggtgc ggctggggcc cagccccagc 1020

tgctcccagt ttttctgct gaccccggtt ccgtgagat cagaaggcaa cagctctgag 1080

ttccaggggc cccaggact gttgtcaggg ccggccccac aaaagcggat ggggggcca 1140

ggcaccccc gagccccaca ccgcctggct ctgccgggcc tcctgcggc cttggagggc 1200

cgcccgagg aggaggagga ggacagtgag gacagcgacg agtctgacga ggagctccgc 1260

tgctacagcg tccaggagcc tagcgaggac agcgaagagg aggcgccggc ggtgcccgctg 1320

gtggtggctg agagccagag cgcgcgaac ctgcgcagcc tgctcaagat gccagcctg 1380

ctgtccgagg cttctgcga ggacctggaa cgcaagaaga aggccgtgtc cttcttcgac 1440

gacgtaccg tctacctctt tgaccaggaa agccccacc gggagctcgg ggagcccttc 1500

ccgggcgcca aggaatcgcc cccacgttc cttaggggga gcccggctc ttccagcgcc 1560

cccaaccggc cgcagcaggc tgatggctcc ccaaattggt ccacagcggg agaggggtgg 1620

gggttcgcgt gggacgacga cttcccgctg atgccggcca aggcagcctt cgccatggcc 1680

ctagaccggg ccgcaccgc cccggctgcg ccacgcccg ctcccttctc gcgcttcacg 1740

gtgtcgcccg cgcccacgtc ccgcttctcc atcacgcacg tgtct 1785

<210> 19

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 19

ggtgagggcc ccggccccgg gccc 24

<210> 20

<211> 18

<212> DNA

<213> Homo sapiens

<400> 20

ggtgagggcc ccggcccc 18

<210> 21

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 21

ggcgagggcc ccggggccc

18

<210> 22

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 22

ctggaggctg aggccgaggc cgag

24

<210> 23

<211> 18

<212> DNA

<213> Homo sapiens

<400> 23

ctcgaggctg aggccgag

18

<210> 24

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 24

ctggaggctg aggccgag

18

<210> 25

<211> 18

<212> DNA

<213> Pan troglodytes

<400> 25

cccacgcccg ctcccttc

18

<210> 26

<211> 24

<212> DNA

<213> Homo sapiens

<400> 26

cccacgcca cgcccgtcc cttc

24

<210> 27

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 27

cccacgcccg ctcccttc

18

<210> 28

<211> 24

<212> DNA

<213> Pan troglodytes

<400> 28

cccacgtcca cgtcccgtt ctcc

24

<210> 29

<211> 18

<212> DNA

<213> Homo sapiens

<400> 29

cccacgtccc gcttctcc

18

<210> 30

<211> 18

<212> DNA

<213> Gorilla gorilla

<400> 30

cccacgtccc gcttctcc

18

<210> 31

<211> 1335

<212> DNA

<213> Pan troglodytes

<400> 31

atggcagtga caactcgttt gacatgggtg catgaaaaga tcctgcaaaa tcatttttga 60

gggaagcggc ttagccttct ctataagggt agtgtccatg gattccataa tggagttttg 120

cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

attggagcat atgcagaaga gggttaccag gmaagaaagt atgcttccat catccttttt 240

gcacttcaag agactaaaat ttcagaatgg aaactaggac tatatacacc agaaacactg 300

ttttgttg acgttgcaaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggacga aagaaagata 480

aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540

ggatccctgg ttcaacaaat acgaattctg ctgctgggtc caattggagc tgggaagtct 600

agctttttca actcagtga gtcgtgtttc caagggcatg taacgcatca ggctttggtg 660

ggcactaata caactgggat atctgagaag tataggacat actctattag agacgggaaa 720

gatggcaa at acctgccatt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780

ggcctgtgca tggatgacat atcctacatc ttgaacggta acattcgtga tagataccag 840

tttaatccca tggaatcaat caaattaaat catcatgact acattgattc cccatcgctg 900

aaggacagaa ttcattgtgt ggcatttgta tttgatgcc gctctattga atacttctcc 960
tctcagatga tagtaaagat caaaagaatt cgaagggagt tggtaaacgc tgggtgtgga 1020
catgtggctt tgctcactca tgtggatagc atggatctga ttacaaaagg tgaccttata 1080
gaaatagaga gatgtgtgcc tgtgaggtcc aagctagagg aagtccaaag aaaacttgga 1140
tttgctcttt ctgacatctc ggtgggttagc aattattcct ctgagtggga gctggaccct 1200
gtaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260
ttagaggatt tgccctttga gcaaataagg aatctaagg aggaaattat caactgtgca 1320
caaggaaaaa aatag 1335

<210> 32

<211> 1335

<212> DNA

<213> Pan troglodytes

<220>

<221> Variation

<222> 212

<223> M= A or C

<400> 32

atg gca gtg aca act cgt ttg aca tgg ttg cat gaa aag atc ctg caa 48
Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1	5	10	15	
aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc				96
Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val				
	20	25	30	
cat gga ttc cat aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg				144
His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly				
	35	40	45	
cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat				192
Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr				
	50	55	60	
gca gaa gag ggt tac cag gma aga aag tat gct tcc atc atc ctt ttt				240
Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe				
65	70	75	80	
gca ctt caa gag act aaa att tca gaa tgg aaa cta gga cta tat aca				288
Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr				
	85	90	95	
cca gaa aca ctg ttt tgt tgt gac gtt gca aaa tat aac tcc cca act				336
Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr				
	100	105	110	
aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag				384
Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys				
	115	120	125	

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag	432
Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln	
130 135 140	
 gat tat gaa gtt ttt cga tgc gaa gat tca ctg gac gaa aga aag ata	480
Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile	
145 150 155 160	
 aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act	528
Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr	
165 170 175	
 tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctg ctg ctg	576
Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu	
180 185 190	
 ggt cca att gga gct ggg aag tct agc ttt ttc aac tca gtg agg tct	624
Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser	
195 200 205	
 gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca	672
Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr	
210 215 220	
 act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa	720
Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys	
225 230 235 240	
 gat ggc aaa tac ctg cca ttt att ctg tgt gac tca ctg ggg ctg agt	768
Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser	
245 250 255	

gag aaa gaa ggc ggc ctg tgc atg gat gac ata tcc tac atc ttg aac	816
Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn	
260 265 270	
ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa	864
Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys	
275 280 285	
tta aat cat cat gac tac att gat tcc cca tgc ctg aag gac aga att	912
Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile	
290 295 300	
cat tgt gtg gca ttt gta ttt gat gcc agc tct att gaa tac ttc tcc	960
His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser	
305 310 315 320	
tct cag atg ata gta aag atc aaa aga att cga agg gag ttg gta aac	1008
Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn	
325 330 335	
gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat	1056
Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp	
340 345 350	
ctg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gtg cct gtg	1104
Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val	
355 360 365	
agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct	1152

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

agg gag gaa att atc aac tgt gca caa gga aaa aaa tag 1335

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

<210> 33

<211> 444

<212> PRT

<213> Pan troglodytes

<220>

<221> Variation

<222> 71

<223> Xaa= Glu or Ala

<400> 33

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

His Gly Phe His Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

Ala Glu Glu Gly Tyr Gln Xaa Arg Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

Ala Leu Gln Glu Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Tyr Thr

85

90

95

Pro Glu Thr Leu Phe Cys Cys Asp Val Ala Lys Tyr Asn Ser Pro Thr

100

105

110

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160

Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165

170

175

Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu
180 185 190

Gly Pro Ile Gly Ala Gly Lys Ser Ser Phe Phe Asn Ser Val Arg Ser
195 200 205

Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr
210 215 220

Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys
225 230 235 240

Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser
245 250 255

Glu Lys Glu Gly Gly Leu Cys Met Asp Asp Ile Ser Tyr Ile Leu Asn
260 265 270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys
275 280 285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile
290 295 300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Glu Tyr Phe Ser
305 310 315 320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Arg Arg Glu Leu Val Asn
325 330 335

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Val Pro Val

355

360

365

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

<210> 34

<211> 1335

<212> DNA

<213> Homo sapiens

<400> 34

atggcagtga caactcgttt gacatggttg cacgaaaaga tcctgcaaaa tcattttgga 60

gggaagcggc ttagccttct ctataagggt agtgtccatg gattccgtaa tggagttttg 120

cttgacagat gttgtaatca agggcctact ctaacagtga tttatagtga agatcatatt 180

attggagcat atgcagaaga gagttaccag gaaggaaagt atgcttccat catccttttt 240

gcacttcaag atactaaaat ttcagaatgg aaactaggac tatgtacacc agaaacactg 300

ttttgttgatg atgttataaa atataactcc ccaactaatt tccagataga tggaagaaat 360

agaaaagtga ttatggactt aaagacaatg gaaaatcttg gacttgctca aaattgtact 420

atctctattc aggattatga agtttttcga tgcgaagatt cactggatga aagaaagata 480

aaaggggtca ttgagctcag gaagagctta ctgtctgcct tgagaactta tgaaccatat 540

ggatccctgg ttcaacaaat acgaattctc ctctgggtc caattggagc tcccaagtcc 600

agctttttca actcagtga gtctgttttc caagggcatg taacgcatca ggctttgggtg 660

ggcactaata caactgggat atctgagaag tataggacat actctattag agacgggaaa 720

gatggcaaat acctgccgtt tattctgtgt gactcactgg ggctgagtga gaaagaaggc 780

ggcctgtgca gggatgacat attctatata ttgaacggtg acattcgtga tagataccag 840

tttaatccca tggaatcaat caaattaaat catcatgact acattgattc cccatcgctg 900

aaggacagaa ttcattgtgt ggcatttgta tttgatgcca gctctattca atacttctcc 960

tctcagatga tagtaaagat caaaagaatt caaaggagat tggtaaacgc tgggtgtggtg 1020

catgtggcctt tgctcactca tgtggatagc atggatttga ttacaaaagg tgaccttata 1080

gaaatagaga gatgtgagcc tgtgaggtec aagctagagg aagtccaaag aaaacttgga 1140

tttgctcttt ctgacatctc ggtgggttagc aattattcct ctgagtggga gctggaccct 1200

gtaaaggatg ttctaattct ttctgctctg agacgaatgc tatgggctgc agatgacttc 1260

ttagaggatt tgccttttga gcaaataagg aatctaaggg aggaaattat caactgtgca 1320

caaggaaaaa aatag 1335

<210> 35

<211> 1335

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1335)

<400> 35

atg gca gtg aca act cgt ttg aca tgg ttg cac gaa aag atc ctg caa 48

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

aat cat ttt gga ggg aag cgg ctt agc ctt ctc tat aag ggt agt gtc 96

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

cat gga ttc cgt aat gga gtt ttg ctt gac aga tgt tgt aat caa ggg 144

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

cct act cta aca gtg att tat agt gaa gat cat att att gga gca tat 192

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

gca gaa gag agt tac cag gaa gga aag tat gct tcc atc atc ctt ttt 240

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

gca ctt caa gat act aaa att tca gaa tgg aaa cta gga cta tgt aca 288

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85

90

95

cca gaa aca ctg ttt tgt tgt gat gtt aca aaa tat aac tcc cca act 336

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100

105

110

aat ttc cag ata gat gga aga aat aga aaa gtg att atg gac tta aag 384

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

aca atg gaa aat ctt gga ctt gct caa aat tgt act atc tct att cag 432

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

gat tat gaa gtt ttt cga tgc gaa gat tca ctg gat gaa aga aag ata 480

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile
 145 150 155 160

aaa ggg gtc att gag ctc agg aag agc tta ctg tct gcc ttg aga act 528
 Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr
 165 170 175

tat gaa cca tat gga tcc ctg gtt caa caa ata cga att ctc ctc ctg 576
 Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu
 180 185 190

ggt cca att gga gct ccc aag tcc agc ttt ttc aac tca gtg agg tct 624
 Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser
 195 200 205

gtt ttc caa ggg cat gta acg cat cag gct ttg gtg ggc act aat aca 672
 Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr
 210 215 220

act ggg ata tct gag aag tat agg aca tac tct att aga gac ggg aaa 720
 Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys
 225 230 235 240

gat ggc aaa tac ctg ccg ttt att ctg tgt gac tca ctg ggg ctg agt 768
 Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser
 245 250 255

gag aaa gaa ggc ggc ctg tgc agg gat gac ata ttc tat atc ttg aac 816
 Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn
 260 265 270

ggt aac att cgt gat aga tac cag ttt aat ccc atg gaa tca atc aaa 864

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

tta aat cat cat gac tac att gat tcc cca tcg ctg aag gac aga att 912

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

cat tgt gtg gca ttt gta ttt gat gcc agc tct att caa tac ttc tcc 960

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser

305

310

315

320

tct cag atg ata gta aag atc aaa aga att caa agg gag ttg gta aac 1008

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn

325

330

335

gct ggt gtg gta cat gtg gct ttg ctc act cat gtg gat agc atg gat 1056

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

ttg att aca aaa ggt gac ctt ata gaa ata gag aga tgt gag cct gtg 1104

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

agg tcc aag cta gag gaa gtc caa aga aaa ctt gga ttt gct ctt tct 1152

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

gac atc tcg gtg gtt agc aat tat tcc tct gag tgg gag ctg gac cct 1200

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400,

gta aag gat gtt cta att ctt tct gct ctg aga cga atg cta tgg gct 1248

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

gca gat gac ttc tta gag gat ttg cct ttt gag caa ata ggg aat cta 1296

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

agg gag gaa att atc aac tgt gca caa gga aaa aaa tag 1335

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440

<210> 36

<211> 444

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Val Thr Thr Arg Leu Thr Trp Leu His Glu Lys Ile Leu Gln

1

5

10

15

Asn His Phe Gly Gly Lys Arg Leu Ser Leu Leu Tyr Lys Gly Ser Val

20

25

30

His Gly Phe Arg Asn Gly Val Leu Leu Asp Arg Cys Cys Asn Gln Gly

35

40

45

Pro Thr Leu Thr Val Ile Tyr Ser Glu Asp His Ile Ile Gly Ala Tyr

50

55

60

Ala Glu Glu Ser Tyr Gln Glu Gly Lys Tyr Ala Ser Ile Ile Leu Phe

65

70

75

80

Ala Leu Gln Asp Thr Lys Ile Ser Glu Trp Lys Leu Gly Leu Cys Thr

85

90

95

Pro Glu Thr Leu Phe Cys Cys Asp Val Thr Lys Tyr Asn Ser Pro Thr

100

105

110

Asn Phe Gln Ile Asp Gly Arg Asn Arg Lys Val Ile Met Asp Leu Lys

115

120

125

Thr Met Glu Asn Leu Gly Leu Ala Gln Asn Cys Thr Ile Ser Ile Gln

130

135

140

Asp Tyr Glu Val Phe Arg Cys Glu Asp Ser Leu Asp Glu Arg Lys Ile

145

150

155

160

Lys Gly Val Ile Glu Leu Arg Lys Ser Leu Leu Ser Ala Leu Arg Thr

165

170

175

Tyr Glu Pro Tyr Gly Ser Leu Val Gln Gln Ile Arg Ile Leu Leu Leu

180

185

190

Gly Pro Ile Gly Ala Pro Lys Ser Ser Phe Phe Asn Ser Val Arg Ser

195

200

205

Val Phe Gln Gly His Val Thr His Gln Ala Leu Val Gly Thr Asn Thr

210

215

220

Thr Gly Ile Ser Glu Lys Tyr Arg Thr Tyr Ser Ile Arg Asp Gly Lys

225

230

235

240

Asp Gly Lys Tyr Leu Pro Phe Ile Leu Cys Asp Ser Leu Gly Leu Ser

245

250

255

Glu Lys Glu Gly Gly Leu Cys Arg Asp Asp Ile Phe Tyr Ile Leu Asn

260

265

270

Gly Asn Ile Arg Asp Arg Tyr Gln Phe Asn Pro Met Glu Ser Ile Lys

275

280

285

Leu Asn His His Asp Tyr Ile Asp Ser Pro Ser Leu Lys Asp Arg Ile

290

295

300

His Cys Val Ala Phe Val Phe Asp Ala Ser Ser Ile Gln Tyr Phe Ser

305

310

315

320

Ser Gln Met Ile Val Lys Ile Lys Arg Ile Gln Arg Glu Leu Val Asn

325

330

335

Ala Gly Val Val His Val Ala Leu Leu Thr His Val Asp Ser Met Asp

340

345

350

Leu Ile Thr Lys Gly Asp Leu Ile Glu Ile Glu Arg Cys Glu Pro Val

355

360

365

Arg Ser Lys Leu Glu Glu Val Gln Arg Lys Leu Gly Phe Ala Leu Ser

370

375

380

Asp Ile Ser Val Val Ser Asn Tyr Ser Ser Glu Trp Glu Leu Asp Pro

385

390

395

400

Val Lys Asp Val Leu Ile Leu Ser Ala Leu Arg Arg Met Leu Trp Ala

405

410

415

Ala Asp Asp Phe Leu Glu Asp Leu Pro Phe Glu Gln Ile Gly Asn Leu

420

425

430

Arg Glu Glu Ile Ile Asn Cys Ala Gln Gly Lys Lys

435

440